0590
0320

Serial Number: 09/988,863A

CRF Processing Date: 3-25-02
Edited by: M. SPENCER
Verified by: _____ (STIC staff)

H#5

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:

ENTERED

_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:

_____

_____

_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING   DATE: 03/25/2002
PATENT APPLICATION: US/09/988,863A   TIME: 09:53:09

        Input Set : A:\pto_ms.txt
        Output Set: N:\CRF3\03252002\I988863A.raw

 3 <110> APPLICANT: Bayer AG
 5 <120> TITLE OF INVENTION: Plant phosphomevalonate kinases
 7 <130> FILE REFERENCE: Le A 35 018
 9 <140> CURRENT APPLICATION NUMBER: US/09/988,863A
10 <141> CURRENT FILING DATE: 2001-11-21
12 <160> NUMBER OF SEQ ID NOS: 5
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2396
18 <212> TYPE: DNA
19 <213> ORGANISM: Arabidopsis thaliana
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (685)..(2199)
25 <400> SEQUENCE: 1
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28 aagcaaactg gggaagatga agatggagtg gtgaagaaca aaaccgtata accgttcggt 120
30 tcagaggtgc cgaaccgaac cgacccgtaa accgaaatcc tcaaaagaaa ttgccgatcg 180
32 gtttgctact gttcaaaacc tcggtgccga gaaccgaaac tgtcggtttt ttcggttcgg 240
34 gtttctcggt ttcttccgaa ctcccaggcc tagtttggtt ttatttttca cgagttttgc 300
36 ttctctttttc atcggcgacg acgacgtcga gtttctgtca aaacgttaac gatccgactc 360
38 gagcgtcgac agtaagagaa gaagacagcg attgtgtgta gatcgacggc gaacgtgtgt 420
40 cgatccgtct cgatcgacgg agaatacgtt tcgatccggt ttcgatccaa atcggagagt 480
42 ttgaggatct aaatcggaaa ttgcattaat actcatctcc aatctcttct gaagagtccg 540
44 aatccgatct accaccacta ctcgtaccgc cggtcattta ctgccgccga tttcaaatta 600
46 tccgatcatt tccggcgata tccaatcgca gactgaggtg aatctggggt tttgatcagc 660
48 gattatcttt gtcactcttt gaaa atg gct gtt gtt gct tct gct cct ggg   711
49   Met Ala Val Val Ala Ser Ala Pro Gly
50   1   5
52 aaa gtt ttg atg act gga ggc tac ctt gta ctc gag aag cca aat gca   759
53 Lys Val Leu Met Thr Gly Gly Tyr Leu Val Leu Glu Lys Pro Asn Ala
54 10   15   20   25
56 ggg ctt gtg ttg agt aca aat gca cgg ttt tac gcg att gtg aag cca   807
57 Gly Leu Val Leu Ser Thr Asn Ala Arg Phe Tyr Ala Ile Val Lys Pro
58   30   35   40
60 atc aac gaa gaa gtc aag cct gaa agt tgg gca tgg aaa tgg aca gat   855
61 Ile Asn Glu Glu Val Lys Pro Glu Ser Trp Ala Trp Lys Trp Thr Asp
62   45   50   55
64 gtc aaa tta aca tca cca cag ctc tcg aga gaa agc atg tat aaa ctg   903
65 Val Lys Leu Thr Ser Pro Gln Leu Ser Arg Glu Ser Met Tyr Lys Leu
66   60   65   70
68 tca ctg aat cat ttg act ctt cag tct gtg tct gca agt gat tca aga   951
69 Ser Leu Asn His Leu Thr Leu Gln Ser Val Ser Ala Ser Asp Ser Arg

RAW SEQUENCE LISTING   DATE: 03/25/2002
PATENT APPLICATION: US/09/988,863A   TIME: 09:53:09

Input Set : A:\pto_ms.txt
Output Set: N:\CRF3\03252002\I988863A.raw

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70      75                  80                  85
72 aac ccc ttt gta gag cat gcg ata cag tat gct ata gct gct gct cat     999
73 Asn Pro Phe Val Glu His Ala Ile Gln Tyr Ala Ile Ala Ala Ala His
74 90                  95                  100                 105
76 ttg gca acc gag aag gac aaa gaa tca ttg cac aaa ctc tta ttg caa     1047
77 Leu Ala Thr Glu Lys Asp Lys Glu Ser Leu His Lys Leu Leu Leu Gln
78                  110                 115                 120
80 ggt ctt gat ata aca ata tta ggc tcc aat gac ttt tac tca tat cgg     1095
81 Gly Leu Asp Ile Thr Ile Leu Gly Ser Asn Asp Phe Tyr Ser Tyr Arg
82                  125                 130                 135
84 aac cag ata gaa tcg gct ggg ctt cca ttg aca cca gaa tcg ctg ggt     1143
85 Asn Gln Ile Glu Ser Ala Gly Leu Pro Leu Thr Pro Glu Ser Leu Gly
86          140                 145                 150
88 acc ctt gca ccg ttt gca tca atc aca ttc aat gct gcg gag tca aat     1191
89 Thr Leu Ala Pro Phe Ala Ser Ile Thr Phe Asn Ala Ala Glu Ser Asn
90      155                 160                 165
92 ggt gct aat tcc aag cct gaa gta gca aaa act ggc tta ggt tct tct     1239
93 Gly Ala Asn Ser Lys Pro Glu Val Ala Lys Thr Gly Leu Gly Ser Ser
94 170                 175                 180                 185
96 gca gca atg aca aca gct gtg gtt gca gct ctg tta cat tat ctt gga     1287
97 Ala Ala Met Thr Thr Ala Val Val Ala Ala Leu Leu His Tyr Leu Gly
98                  190                 195                 200
100 gtg gtt gac cta tct gat cca tgt aaa gaa gga aag ttt ggc tgt tct    1335
101 Val Val Asp Leu Ser Asp Pro Cys Lys Glu Gly Lys Phe Gly Cys Ser
102          205                 210                 215
104 gat cta gat gtt atc cat atg ata gca caa acg tct cat tgt ctt gca    1383
105 Asp Leu Asp Val Ile His Met Ile Ala Gln Thr Ser His Cys Leu Ala
106          220                 225                 230
108 caa ggg aag gtc gga agt ggg ttt gat gtc agc tgt gct gtc tat gga    1431
109 Gln Gly Lys Val Gly Ser Gly Phe Asp Val Ser Cys Ala Val Tyr Gly
110     235                 240                 245
112 agt cag cgt tat gtt cgc ttc tct cca gaa gtc ttg tca ttt gct cag    1479
113 Ser Gln Arg Tyr Val Arg Phe Ser Pro Glu Val Leu Ser Phe Ala Gln
114 250                 255                 260                 265
116 gtt gca gta aca ggt ctg cca tta aat gaa gtt att ggt aca att ttg    1527
117 Val Ala Val Thr Gly Leu Pro Leu Asn Glu Val Ile Gly Thr Ile Leu
118                  270                 275                 280
120 aag gga aaa tgg gac aat aag aga act gag ttc tct tta cca cca ctg    1575
121 Lys Gly Lys Trp Asp Asn Lys Arg Thr Glu Phe Ser Leu Pro Pro Leu
122          285                 290                 295
124 atg aat ctt ttc ctt gga gaa cct gga agt ggt gga tcc tcc aca cca    1623
125 Met Asn Leu Phe Leu Gly Glu Pro Gly Ser Gly Gly Ser Ser Thr Pro
126          300                 305                 310
128 tca atg gta ggt gca gta aag aag tgg caa atg tct gat cca gag aag    1671
129 Ser Met Val Gly Ala Val Lys Lys Trp Gln Met Ser Asp Pro Glu Lys
130     315                 320                 325
132 gca cga gaa aac tgg cag aat ttg tca gat gca aat tta gaa ctg gaa    1719
133 Ala Arg Glu Asn Trp Gln Asn Leu Ser Asp Ala Asn Leu Glu Leu Glu
134 330                 335                 340                 345
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PATENT APPLICATION: US/09/988,863A   TIME: 09:53:09

Input Set : A:\pto_ms.txt
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136 act aag cta aac gat ctg agc aaa tta gct aaa gac cac tgg gat gtt   1767
137 Thr Lys Leu Asn Asp Leu Ser Lys Leu Ala Lys Asp His Trp Asp Val
138             350             355             360
140 tat cta cga gtc att aag tct tgt agt gtg ctt act tct gaa aag tgg   1815
141 Tyr Leu Arg Val Ile Lys Ser Cys Ser Val Leu Thr Ser Glu Lys Trp
142             365             370             375
144 gtg tta cat gct act gaa cca atc aac gaa gcc att att aaa gaa ctc   1863
145 Val Leu His Ala Thr Glu Pro Ile Asn Glu Ala Ile Ile Lys Glu Leu
146             380             385             390
148 tta gag gca aga gaa gct atg ttg agg atc aga att ctt atg cgt cag   1911
149 Leu Glu Ala Arg Glu Ala Met Leu Arg Ile Arg Ile Leu Met Arg Gln
150     395             400             405
152 atg ggt gag gcg gct agc gtt ccg ata gag cct gaa tct caa act caa   1959
153 Met Gly Glu Ala Ala Ser Val Pro Ile Glu Pro Glu Ser Gln Thr Gln
154 410             415             420                 425
156 ctt ttg gat tct aca atg agt gct gaa gga gtt cta ctt gct ggt gtt   2007
157 Leu Leu Asp Ser Thr Met Ser Ala Glu Gly Val Leu Leu Ala Gly Val
158             430             435             440
160 cct gga gct ggt gga ttt gat gcc ata ttt gca atc act tta ggg gat   2055
161 Pro Gly Ala Gly Gly Phe Asp Ala Ile Phe Ala Ile Thr Leu Gly Asp
162             445             450             455
164 tcc ggc acc aaa ctg acc cag gca tgg agt tcg cac aat gtt ttg gcc   2103
165 Ser Gly Thr Lys Leu Thr Gln Ala Trp Ser Ser His Asn Val Leu Ala
166             460             465             470
168 ttg ttg gtg aga gaa gat cca cat ggc gtt tgc cta gaa agt ggt gat   2151
169 Leu Leu Val Arg Glu Asp Pro His Gly Val Cys Leu Glu Ser Gly Asp
170     475             480             485
172 cca cga acc aca tgt att act tca ggc gtt tca tca att cac ctt gag   2199
173 Pro Arg Thr Thr Cys Ile Thr Ser Gly Val Ser Ser Ile His Leu Glu
174 490             495             500                 505
176 taaacaacat tgtttcagtg tccaattatt aggtgcgtca ccaagttcgg ttgagtatac 2259
178 tgttttgcat atagacttgg gtgctaaatt tcttggtgta agcatttta tacccattgt 2319
180 aaggtcttta actcttggaa aacttgcggg aaaataaaat aaagttgatt tcaaatcttc 2379
182 tcaaaaaaaa aaaaaaa                                                2396
185 <210> SEQ ID NO: 2
186 <211> LENGTH: 505
187 <212> TYPE: PRT
188 <213> ORGANISM: Arabidopsis thaliana
190 <400> SEQUENCE: 2
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192   1             5             10              15
194 Tyr Leu Val Leu Glu Lys Pro Asn Ala Gly Leu Val Leu Ser Thr Asn
195             20             25              30
197 Ala Arg Phe Tyr Ala Ile Val Lys Pro Ile Asn Glu Glu Val Lys Pro
198             35             40              45
200 Glu Ser Trp Ala Trp Lys Trp Thr Asp Val Lys Leu Thr Ser Pro Gln
201     50             55             60
203 Leu Ser Arg Glu Ser Met Tyr Lys Leu Ser Leu Asn His Leu Thr Leu
204 65             70             75              80
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RAW SEQUENCE LISTING   DATE: 03/25/2002
PATENT APPLICATION: US/09/988,863A   TIME: 09:53:10

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Output Set: N:\CRF3\03252002\I988863A.raw

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206 Gln Ser Val Ser Ala Ser Asp Ser Arg Asn Pro Phe Val Glu His Ala
207               85                  90                  95
209 Ile Gln Tyr Ala Ile Ala Ala Ala His Leu Ala Thr Glu Lys Asp Lys
210              100             105             110
212 Glu Ser Leu His Lys Leu Leu Leu Gln Gly Leu Asp Ile Thr Ile Leu
213          115             120             125
215 Gly Ser Asn Asp Phe Tyr Ser Tyr Arg Asn Gln Ile Glu Ser Ala Gly
216      130             135             140
218 Leu Pro Leu Thr Pro Glu Ser Leu Gly Thr Leu Ala Pro Phe Ala Ser
219 145             150             155                 160
221 Ile Thr Phe Asn Ala Ala Glu Ser Asn Gly Ala Asn Ser Lys Pro Glu
222              165             170             175
224 Val Ala Lys Thr Gly Leu Gly Ser Ser Ala Ala Met Thr Thr Ala Val
225              180             185             190
227 Val Ala Ala Leu Leu His Tyr Leu Gly Val Val Asp Leu Ser Asp Pro
228          195             200             205
230 Cys Lys Glu Gly Lys Phe Gly Cys Ser Asp Leu Asp Val Ile His Met
231      210             215             220
233 Ile Ala Gln Thr Ser His Cys Leu Ala Gln Gly Lys Val Gly Ser Gly
234 225             230             235                 240
236 Phe Asp Val Ser Cys Ala Val Tyr Gly Ser Gln Arg Tyr Val Arg Phe
237              245             250             255
239 Ser Pro Glu Val Leu Ser Phe Ala Gln Val Ala Val Thr Gly Leu Pro
240              260             265             270
242 Leu Asn Glu Val Ile Gly Thr Ile Leu Lys Gly Lys Trp Asp Asn Lys
243          275             280             285
245 Arg Thr Glu Phe Ser Leu Pro Pro Leu Met Asn Leu Phe Leu Gly Glu
246      290             295             300
248 Pro Gly Ser Gly Gly Ser Ser Thr Pro Ser Met Val Gly Ala Val Lys
249 305             310             315                 320
251 Lys Trp Gln Met Ser Asp Pro Glu Lys Ala Arg Glu Asn Trp Gln Asn
252              325             330             335
254 Leu Ser Asp Ala Asn Leu Glu Leu Glu Thr Lys Leu Asn Asp Leu Ser
255              340             345             350
257 Lys Leu Ala Lys Asp His Trp Asp Val Tyr Leu Arg Val Ile Lys Ser
258          355             360             365
260 Cys Ser Val Leu Thr Ser Glu Lys Trp Val Leu His Ala Thr Glu Pro
261      370             375             380
263 Ile Asn Glu Ala Ile Ile Lys Glu Leu Leu Glu Ala Arg Glu Ala Met
264 385             390             395                 400
266 Leu Arg Ile Arg Ile Leu Met Arg Gln Met Gly Glu Ala Ala Ser Val
267              405             410             415
269 Pro Ile Glu Pro Glu Ser Gln Thr Gln Leu Leu Asp Ser Thr Met Ser
270              420             425             430
272 Ala Glu Gly Val Leu Leu Ala Gly Val Pro Gly Ala Gly Gly Phe Asp
273          435             440             445
275 Ala Ile Phe Ala Ile Thr Leu Gly Asp Ser Gly Thr Lys Leu Thr Gln
276      450             455             460
278 Ala Trp Ser Ser His Asn Val Leu Ala Leu Leu Val Arg Glu Asp Pro
```

```
279 465                     470               475                    480
281 His Gly Val Cys Leu Glu Ser Gly Asp Pro Arg Thr Thr Cys Ile Thr
282                 485                       490                    495
284 Ser Gly Val Ser Ser Ile His Leu Glu
285             500                 505
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290 <211> LENGTH: 611
291 <212> TYPE: DNA
292 <213> ORGANISM: Medicago truncatula
294 <400> SEQUENCE: 3
295 ctgttatctg agttgaagaa atatcacaat atcaatggcc gtggtggttg cttctgctcc 60
296 tgggaaggtg ttaatgaccg gtggctacct agttttagag agacctaatg ctggacttgt 120
297 tcttagtact aatgctcgtt tttatgctat tgtcaaacca atctatcctc aaactaaacc 180
298 tgattcttgg gcttgggctt ggtcagatgt cagattaaca tctcctcaac tctccagaga 240
299 agccttctat aaattagcac tcaaaaatct taccatccaa actgtttcct caagtgaaac 300
300 aaggaaccct tttgtggaat atgctgtgca atactccgtg gctgccgcct atgcaacagc 360
301 tgaccagaat aaaaaggact tgttgcacaa actacttttg caaggtcttg acattacaat 420
302 tttgggttcc aatgattttt attcttatag gaatgagatt gagagacacg gactcccttt 480
303 gacatcagaa tcattggcca cccttccgcc ttttgcctcc atttctttca atactgatga 540
304 tgctaatgga aggaattgta agcctgaaat tgccaaaact ggtttgggct catctgcagc 600
305 aatgacaacc g                                                     611
308 <210> SEQ ID NO: 4
309 <211> LENGTH: 728
310 <212> TYPE: DNA
311 <213> ORGANISM: Gossypium hirsutum
312 <220> FEATURE:
313 <221> NAME/KEY: unsure
314 <222> LOCATION: 715
315 <223> OTHER INFORMATION: n can be any nucleotide
318 <400> SEQUENCE: 4
319 cgttttttacg ctattgttaa gccaattcat gaagctatca agcctgaaag ctgggcatgg 60
320 tcttggaccg atgtcaagct aacatctcct cagctttcca gagaaagcat gtataaattg 120
321 tctcggaaac atttaacact tcagtgtgta tcttcaagtg aatcaaggaa cccttttgta 180
322 gaaatgcta ttcaatatac tatagcagct gcacatgcaa catttgacaa gaataagaaa 240
323 gaggcattag ataaactact cttacaaggt cttgatatta cgatcttagg ttgcaatgac 300
324 ttttactcat acaggaatca gatagaagca cttggtcttc cgttgacacc tgaagcattg 360
325 gctactctac caccgtttac atcaattaca ttcaattctg aggaatcaaa tggagcaaat 420
326 tgcaaacctg aagttgcaaa aactggattg ggttcatctg cagcaatgac aactgctgta 480
327 gttgctgctt tacttcatta tcttggtgtt gttaacccttt ccacctcttc tgcagatcaa 540
328 caccaagaaa ataagaattc cacagatctc gatattgtgc atatgatagc tcaaagtgcc 600
329 cactgtattg cccaaggtaa agttggcagt ggctttgatg tcagttctgc tgtctatggg 660
330 agtcagcgtt atgttcgttt ttcaccaaaa gtgctttctg ctgctcaggc tgcantgaaa 720
331 gggatgcc                                                        728
334 <210> SEQ ID NO: 5
335 <211> LENGTH: 571
336 <212> TYPE: DNA
337 <213> ORGANISM: Pinus radiata
339 <400> SEQUENCE: 5
340 cacaggcgaa accctctcct gctgctcacg gttgataaac cctcaatatt tgcggtaggg 60
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W--> 312
W--> 330

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/988,863A

DATE: 03/25/2002
TIME: 09:53:11

Input Set : **A:\pto_ms.txt**
Output Set: **N:\CRF3\03252002\I988863A.raw**

L:312 M:283 W: Missing Blank Line separator, <220> field identifier
L:330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4